

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/603,208

DATE: 07/07/2000
 TIME: 13:19:05

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\07072000\I603208.raw

PS. 4

**Does Not Comply
 Corrected Diskette Needed**

3 <110> APPLICANT: Pompejus, Markus
 4 Kroger, Burkhard
 5 Schroder, Hartwig
 6 Zelder, Oskar
 7 Haberhauer, Gregor
 8 Lee, Heung-Shick
 9 Kim, Hyung-Joon
 W--> 10 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
 W--> 11 RESISTANCE AND TOLERANCE PROTEINS
 W--> 12 <130> FILE REFERENCE: BGI-124CP
 W--> 13 <140> CURRENT APPLICATION NUMBER:
 C--> 14 <141> CURRENT FILING DATE: 2000-06-23
 W--> 15 <160> NUMBER OF SEQ ID: 304
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1566
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Corynebacterium glutamicum
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (101)..(1543)
 25 <223> OTHER INFORMATION: RXA01524
 27 <400> SEQUENCE: 1
 28 ttgtggcact ctttagtagt tttttctcat agctcagttt cgcaacttta gagaactcta 60
 30 gaaactgagc ttcattgctgt gaaaggcctt ttctccattc atg gat tcc caa att 115
 31 Met Asp Ser Gln Ile
 32 1 5
 34 aat act cag acc tct ccg gca gct gcg aag ctg cct agg gag gtc gtt 163
 35 Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu Pro Arg Glu Val Val
 36 10 15 20
 38 gtt gtt ctt tcg atc ctc gtg gtt tcc gcg atg atc atg att ctt aat 211
 39 Val Val Leu Ser Ile Leu Val Val Ser Ala Met Ile Met Ile Leu Asn
 40 25 30 35
 42 gaa acc att ctg tcg gtt gcg ttg cct tcc atc atg gaa gat ttc tcc 259
 43 Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile Met Glu Asp Phe Ser
 44 40 45 50
 46 gtg cct gaa act act gca cag tgg ttg acc act ggc ttt atg ttg acg 307
 47 Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr Gly Phe Met Leu Thr
 48 55 60 65
 50 atg gca gtg gtg att cca act act ggt tat ctg ctt gat cgt ttt tcc 355
 51 Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu Leu Asp Arg Phe Ser
 52 70 75 80 85
 54 act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg 403
 55 Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
 56 90 95 100
 58 ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt 451
 59 Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
 60 105 110 115

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```

62 atc gtt cag gcg gtt ggt act gcg ctg gtg atg cct ttg ctg atg acg 499
63 Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr
64      120      125      130
66 gtt acg ttg acg gtg gtt cct gcg gag cgt cgt ggt tcg atg atg ggc 547
67 Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg Gly Ser Met Met Gly
68      135      140      145
70 att att tcc atc gtg att tct gtt gcg ccg gcg ctt ggt cct acg ttg 595
71 Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala Leu Gly Pro Thr Leu
72 150      155      160      165
74 tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg 643
75 Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met
76      170      175      180
78 atg ctt ccg atc gtt gtt atc gct ttg gta att ggt ttc ttc ttg atc 691
79 Met Leu Pro Ile Val Val Ile Ala Leu Val Ile Gly Phe Phe Leu Ile
80      185      190      195
82 aaa aat atc ggc gaa acc aag atc acc cca ctg gat gtt ctg tct gtc 739
83 Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu Asp Val Leu Ser Val
84      200      205      210
86 atc ctt tcg gtg ttt gcc ttc ggt ggt ttg gtg tac ggc ttc agt tcc 787
87 Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val Tyr Gly Phe Ser Ser
88      215      220      225
90 ttc gga gca atc ctg gag ggc gaa ggc acc gta ggt atc ttc gcg atc 835
91 Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val Gly Ile Phe Ala Ile
92 230      235      240      245
94 gtc gtt ggc gcc atc gca ctc ctc atc ttt gct ttg cga cag cac caa 883
95 Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala Leu Arg Gln His Gln
96      250      255      260
98 ctc ggc aag caa gac aaa gca ctg atg gat ctc cga gcc ttc aag gtg 931
99 Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu Arg Ala Phe Lys Val
100      265      270      275
102 agg aac ttc agc ttc tcc ttg acc acc atc ctt ttg gcg ttc ggc gcg 979
103 Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu Leu Ala Phe Gly Ala
104      280      285      290
106 atg ctc gga acc gtc atg gtt ttg cca atc tac ctg cag act tcc ctc 1027
107 Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr Leu Gln Thr Ser Leu
108      295      300      305
110 gga gtt act gct ttg gtg acc ggt ttg gtt gtt atg ccc ggc ggc ctc 1075
111 Gly Val Thr Ala Leu Val Thr Gly Leu Val Val Met Pro Gly Gly Leu
112 310      315      320      325
114 ctc cag ggt ctg atc agc cca ttc atc gga cgt ttc tac gac aag gtc 1123
115 Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg Phe Tyr Asp Lys Val
116      330      335      340
118 ggt cca cgt ccg ctg ctg att ccc gga gca att gcg ctg gct atc gcg 1171
119 Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile Ala Leu Ala Ile Ala
120      345      350      355
122 gca tcc tcg atg act ttt ctc aat gag aat tca ccc gtg tgg atg gtc 1219
123 Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser Pro Val Trp Met Val
124      360      365      370
126 gtg gtc atg cac gtt gtg ttc agc atc ggc atg tgt ttg atg atg acc 1267

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```

127 Val Val Met His Val Val Phe Ser Ile Gly Met Cys Leu Met Met Thr
128      375      380      385
130 cct ctc atg acc acc gct ctc ggc gcc ctt ccg aag cac ctc tat ggt 1315
131 Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro Lys His Leu Tyr Gly
132 390      395      400      405
134 cac ggc tcc gca att ttg aac acg ttc caa cag ctc gca ggc gca gcc 1363
135 His Gly Ser Ala Ile Leu Asn Thr Phe Gln Leu Ala Gly Ala Ala
136      410      415      420
138 gga aca gcg atc atg att gca gca ctt tcc ttc ggc act tcc att gca 1411
139 Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe Gly Thr Ser Ile Ala
140      425      430      435
142 gcg tct tcg gga tct gcg cat gct gaa gct gtt gcc gct ggt acc aag 1459
143 Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val Ala Ala Gly Thr Lys
144      440      445      450
146 gtt gcg ttc atc gca ggc gca atc atc gcg gtg atc gct ttg gtt gtt 1507
147 Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val Ile Ala Leu Val Val
148      455      460      465
150 tcc ctc ttc gtc act cgc gtc gag gaa gaa gct cac taaataccaa 1553
151 Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala His
152 470      475      480
154 aaaatggggc aga 1566
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 481
159 <212> TYPE: PRT
160 <213> ORGANISM: Corynebacterium glutamicum
162 <400> SEQUENCE: 2
163 Met Asp Ser Gln Ile Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu
164 1      5      10      15
166 Pro Arg Glu Val Val Val Val Leu Ser Ile Leu Val Val Ser Ala Met
167      20      25      30
169 Ile Met Ile Leu Asn Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile
170      35      40      45
172 Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
173      50      55      60
175 Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
176 65      70      75      80
178 Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
179      85      90      95
181 Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
182      100      105      110
184 Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
185      115      120      125
187 Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
188      130      135      140
190 Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
191 145      150      155      160
193 Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
194      165      170      175
196 Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile

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```

197          180          185          190
199 Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
200          195          200          205
202 Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
203          210          215          220
205 Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
206 225          230          235          240
208 Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
209          245          250          255
211 Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
212          260          265          270
214 Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
215          275          280          285
217 Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
218          290          295          300
220 Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
221 305          310          315          320
223 Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
224          325          330          335
226 Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
227          340          345          350
229 Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
230          355          360          365
232 Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
233          370          375          380
235 Cys Leu Met Met Thr Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro
236 385          390          395          400
238 Lys His Leu Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln
239          405          410          415
241 Leu Ala Gly Ala Ala Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe
242          420          425          430
244 Gly Thr Ser Ile Ala Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val
245          435          440          445
247 Ala Ala Gly Thr Lys Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val
248          450          455          460
250 Ile Ala Leu Val Val Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala
251 465          470          475          480
253 His
257 <210> SEQ ID NO: 3
258 <211> LENGTH: 371
259 <212> TYPE: DNA
260 <213> ORGANISM: Corynebacterium glutamicum
262 <220> FEATURE:
263 <221> NAME/KEY: CDS
264 <222> LOCATION: (52)..(348)
265 <223> OTHER INFORMATION: RXA00497
267 <400> SEQUENCE: 3
268 tggaaaccga caaccggcac acacaaaatt tttctcatgg agggattcac cgtg gca 57
W--> 269 Val Ala

```

insert a space after 'c', since
 it is not
 included in
 the triplet (codon)
 of gtg. Per 1.822
 of sequence rules,
 "... Leftover bases,
 fewer than 10 in number,
 ... shall be ... separated
 from adjacent groups of
 10 or 3 bases by a space."

Please correct similar subsequent sequence

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```

270                                     1
272 aac gtc aac atc aag ccg ctt gag gac aag atc ctc gtt cag atc aac 105
273 Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln Ile Asn
274                                     5          10          15
276 gaa gca gag acc acc acc gct tcc gcc ctg gtc att cca gat tcc gct 153
277 Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp Ser Ala
278          20          25          30
280 aag gaa aag cca caa gag gca acc gtt atc gca gtt gcc cca gcc cgc 201
281 Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro Gly Arg
282          35          40          45          50
284 ttc gat gac aag ggt aac cgc atc cca ctg gac atc aag gaa gat gac 249
285 Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu Asp Asp
286          55          60          65
288 gtt gtg atc ttc tcc cgt tac gcc gcc acc gag atc aag ttc ggt gcc 297
289 Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe Gly Gly
290          70          75          80
292 gtg gag tac ttg ctt ctc tcc gct cgt gac atc ctc gca atc gtc gag 345
293 Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile Val Glu
294          85          90          95
296 aag taggggataa gttcatggca aag 371
297 Lys
301 <210> SEQ ID NO: 4
302 <211> LENGTH: 99
303 <212> TYPE: PRT
304 <213> ORGANISM: Corynebacterium glutamicum
306 <400> SEQUENCE: 4
307 Val Ala Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln
308          1          5          10          15
310 Ile Asn Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp
311          20          25          30
313 Ser Ala Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro
314          35          40          45
316 Gly Arg Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu
317          50          55          60
319 Asp Asp Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe
320          65          70          75          80
322 Gly Gly Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile
323          85          90          95
325 Val Glu Lys
329 <210> SEQ ID NO: 5
330 <211> LENGTH: 1737
331 <212> TYPE: DNA
332 <213> ORGANISM: Corynebacterium glutamicum
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (101)..(1714)
337 <223> OTHER INFORMATION: RXN00493
339 <400> SEQUENCE: 5
340 cccgttacgg cggcaccgag atcaagttcg gtggcgtgga gtacttgctt ctctccgctc 60

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

PSI
✓

VERIFICATION SUMMARY

DATE: 07/07/2000

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Input Set : A:\seqlist.txt

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L:10 M:283 W: Missing Blank Line separator, <120> field identifier
L:12 M:283 W: Missing Blank Line separator, <130> field identifier
L:13 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:269 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 3, CDS LOCATION:52..348
L:927 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 11, CDS LOCATION:33..1580
L:3046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:3047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:3050 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:3051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:3174 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:3174 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:3174 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:3174 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34
L:3174 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:3177 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:3177 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:3177 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:3177 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:4158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:4166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:4170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:4173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:4174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:4212 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:4212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:4212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:4212 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
L:4212 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46
L:4218 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:4218 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:4218 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:4218 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
M:340 Repeated in SeqNo=46
L:4221 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:4221 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:4221 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:4221 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
L:4224 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:4224 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:4224 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:4224 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
L:4242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:4244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:4245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:4268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47

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L:4269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:4272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:4283 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:4283 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:4283 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:4283 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
L:4283 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:48
L:4301 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:4301 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:4301 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:4301 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
M:340 Repeated in SeqNo=48
L:5505 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 61, CDS LOCATION:48..1196
L:20067 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 257, CDS LOCATION:93..1487
L:21795 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 275, CDS LOCATION:65..511
L:23650 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:302
L:23650 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:302
L:23650 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:302
L:23650 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:302
L:23650 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:302